

SEQUENCE LISTING

<110> SIRS-Lab GmbH

5 <120> Method of enriching/separating prokaryotic DNA by means of
a protein which specifically binds DNA containing non-methylated
CpG motifs

<130> Pat 3696/29-PCT

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<170> PatentIn Ver. 2.1

<210> 1

<211> 543

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<212> DNA

<213> Homo sapiens

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<221> CDS

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gca ggg tca ggg aca ggg gtt ggg gcc atg ctt gct cgg ggc tct gct 96
Ala Gly Ser Gly Thr Gly Val Gly Ala Met Leu Ala Arg Gly Ser Ala
20 25 30

35

tcg ccc cac aaa tcc tct ccg cag ccc ttg gtg gcc aca ccc agc cag 144
Ser Pro His Lys Ser Ser Pro Gln Pro Leu Val Ala Thr Pro Ser Gln
35 40 45

40

cat cac cag cag cag cag cag cag atc aaa cgg tca gcc cgc atg tgt 192
His His Gln Gln Gln Gln Gln Gln Ile Lys Arg Ser Ala Arg Met Cys
50 55 60

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ggt gag tgt gag gca tgt cgg cgc act gag gac tgt ggt cac tgt gat 240
Gly Glu Cys Glu Ala Cys Arg Arg Thr Glu Asp Cys Gly His Cys Asp
65 70 75 80

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ttc tgt cgg gac atg aag aag ttc ggg ggc ccc aac aag atc cgg cag 288
Phe Cys Arg Asp Met Lys Lys Phe Gly Gly Pro Asn Lys Ile Arg Gln
85 90 95

55

aag tgc cgg ctg cgc cag tgc cag ctg cgg gcc cgg gaa tcg tac aag 336
Lys Cys Arg Leu Arg Gln Cys Gln Leu Arg Ala Arg Glu Ser Tyr Lys
100 105 110

tac ttc cct tcc tcg ctc tca cca gtg acg ccc tca gag tcc ctg cca 384
Tyr Phe Pro Ser Ser Leu Ser Pro Val Thr Pro Ser Glu Ser Leu Pro
115 120 125

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    agg ccc cgc cgg cca ctg ccc acc caa cag cag cca cag cca tca cag 432
    Arg Pro Arg Arg Pro Leu Pro Thr Gln Gln Gln Pro Gln Pro Ser Gln
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5    aag tta ggg cgc atc cgt gaa gat gag ggg gca gtg gcg tca tca aca 480
    Lys Leu Gly Arg Ile Arg Glu Asp Glu Gly Ala Val Ala Ser Ser Thr
    145              150              155              160

10   gtc aag gag cct cct gag gct aca gcc aca cct gag cca ctc tca gat 528
    Val Lys Glu Pro Pro Glu Ala Thr Ala Thr Pro Glu Pro Leu Ser Asp
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    gag gac cta cct ctg 543
15   Glu Asp Leu Pro Leu
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    Ala Gly Ser Gly Thr Gly Val Gly Ala Met Leu Ala Arg Gly Ser Ala
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30   Ser Pro His Lys Ser Ser Pro Gln Pro Leu Val Ala Thr Pro Ser Gln
      35              40              45

    His His Gln Gln Gln Gln Gln Gln Ile Lys Arg Ser Ala Arg Met Cys
35   50              55              60

    Gly Glu Cys Glu Ala Cys Arg Arg Thr Glu Asp Cys Gly His Cys Asp
      65              70              75              80

40   Phe Cys Arg Asp Met Lys Lys Phe Gly Gly Pro Asn Lys Ile Arg Gln
      85              90              95

    Lys Cys Arg Leu Arg Gln Cys Gln Leu Arg Ala Arg Glu Ser Tyr Lys
      100              105              110

45   Tyr Phe Pro Ser Ser Leu Ser Pro Val Thr Pro Ser Glu Ser Leu Pro
      115              120              125

    Arg Pro Arg Arg Pro Leu Pro Thr Gln Gln Gln Pro Gln Pro Ser Gln
50   130              135              140

    Lys Leu Gly Arg Ile Arg Glu Asp Glu Gly Ala Val Ala Ser Ser Thr
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55   Val Lys Glu Pro Pro Glu Ala Thr Ala Thr Pro Glu Pro Leu Ser Asp
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    Glu Asp Leu Pro Leu

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